CLAIMS

WE CLAIM:

1. An isolated nucleic acid molecule having a polymorphic site and comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-22 and the complements thereof.

2. An isolated nucleic acid molecule comprising a portion of a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-22 and the complements thereof which is at least 10 nucleotides in length and comprises a polymorphic site.

3. An isolated nucleic acid molecule according to Claim 1, wherein the nucleotide at the polymorphic site is different from the nucleotide at the polymorphic site in a corresponding reference allele.

4. An isolated allele-specific oligonucleotide which hybridizes to a nucleic acid molecule having a polymorphic site and comprising a nucleic acid sequence selected from the group consisting of SEQ ID NOS: 1-22 and the complements thereof under high stringency conditions.

5. An isolated allele-specific oligonucleotide according to Claim 4, which is at least 10 nucleotides in length.

6. An isolated allele-specific oligonucleotide according to Claim 4, in which a nucleotide occupying a central position of said oligonucleotide aligns with and is complementary to a nucleotide occupying the polymorphic site of the nucleic acid molecule to which it hybridizes.

7. An isolated allele-specific oligonucleotide according to Claim 4, in which a nucleotide occupying the 3' end of said oligonucleotide aligns with and is complementary to a nucleotide occupying the polymorphic site of the nucleic acid molecule to which it hybridizes.

8. An isolated peptide encoded by a nucleic acid molecule according to Claim 1.

9. A method of analyzing a nucleic acid sample for polymorphisms, comprising the steps of:

(a) obtaining a nucleic acid sample from one or more individuals, and

(b) determining the nucleotide occupying one or more of the polymorphic sites of one or more nucleic acid molecules selected from the group consisting of SEQ ID NOS: 1-22.

10. A method according to Claim 9, wherein the nucleic acid sample is obtained from a plurality of individuals, and the nucleotide occupying one or more of the polymorphic sites is determined in each of the individuals.

11. A method according to Claim 9, further comprising testing each individual for the presence of a disease phenotype and correlating the presence of the disease phenotype with the nucleotide present at one or more polymorphic sites.

12. A method for predicting the likelihood that an individual will have a cardiovascular disease, comprising the steps of:

(a) obtaining a nucleic acid sample from an individual to be assessed; and

(b) determining the nucleotide present at a polymorphic site of one or more nucleic acid molecules having a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-22,

wherein the presence of a nucleotide associated with a lower likelihood of having a cardiovascular disease indicates that the individual has a lower likelihood of having a cardiovascular disease than if another nucleotide was present at the polymorphic site.

13. A method according to Claim 12, wherein the cardiovascular disease is coronary heart disease.

14. A method for predicting the likelihood that an individual will have a cardiovascular disease, comprising the steps of:

(a) obtaining a nucleic acid sample from an individual to be assessed; and

(b) determining the nucleotide present at a polymorphic site of one or more nucleic acid molecules having a nucleotide sequence selected from the group consisting of SEQ ID NOS: 1-22,

wherein the presence of a nucleotide associated with a greater likelihood of having a cardiovascular disease indicates that the individual has a greater likelihood of having a cardiovascular disease than if another nucleotide was present at the polymorphic site.

15. A method according to Claim 14, wherein the cardiovascular disease is coronary heart disease.